

--ABSTRACT OF THE DISCLOSURE

A method for the development of gene panels for diagnostic and therapeutic purposes comprising the steps of: (a) isolating at least one biological sample from each of at least two groups of biological material containing mRNA and/or proteins; (b) analyzing the expression level of at least one gene in the at least one biological sample; (c) selecting the gene(s) exhibiting a different expression level between the at least two groups of biological material, whereby a first knowledge base is generated; (d) analyzing the level of cytosine methylation in the methylation relevant regions of at least one gene of at least one of the biological samples of step (a), wherein the gene is selected on the basis of the first knowledge base; (e) selecting the gene(s) exhibiting a different level of cytosine methylation between the at least two groups of biological material, whereby a second knowledge base is generated; and (f) adding selected genes from the second knowledge base to a gene panel.--